

Search for

Limits

Preview/Index

History

Clipboard

Details

Display Show

Range: from to ☐ Reverse complemented strand Features:
☐ 1: [NM_080751](#). Reports Homo sapiens tran...[gi:94536851]

[Links](#)
[Comment](#) [Features](#) [Sequence](#)

LOCUS NM_080751 3169 bp mRNA linear PRI 14-MAY-2006
 DEFINITION Homo sapiens transmembrane channel-like 2 (TMC2), mRNA.
 ACCESSION NM_080751
 VERSION NM_080751.2 GI:94536851
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3169)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification of transcriptional modulation: large-scale
 identification and characterization of putative alternative
 promoters of human genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 REFERENCE 2 (bases 1 to 3169)
 AUTHORS Kurima,K., Yang,Y., Sorber,K. and Griffith,A.J.
 TITLE Characterization of the transmembrane channel-like (TMC) gene
 family: functional clues from hearing loss and epidermodysplasia
 verruciformis
 JOURNAL Genomics 82 (3), 300-308 (2003)
 PUBMED 12906855
 REFERENCE 3 (bases 1 to 3169)
 AUTHORS Keresztes,G., Mutai,H. and Heller,S.
 TITLE TMC and EVER genes belong to a larger novel family, the TMC gene
 family encoding transmembrane proteins
 JOURNAL (er) BMC Genomics 4 (1), 24 (2003)
 PUBMED 12812529
 REFERENCE 4 (bases 1 to 3169)
 AUTHORS Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
 Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.,
 Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Riazuddin,S.,
 Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F. Jr.,
 Keats,B.J., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
 TITLE Dominant and recessive deafness caused by mutations of a novel
 gene, TMCL1, required for cochlear hair-cell function
 JOURNAL Nat. Genet. 30 (3), 277-284 (2002)
 PUBMED 11850618
 COMMENT VALIDATED [REFSEQ](#): This record has undergone preliminary review of
 the sequence, but has not yet been subject to final review. The
 reference sequence was derived from [AF417580.2](#), [DA769512.1](#) and
[AL049712.12](#).
 On May 4, 2006 this sequence version replaced gi:[20304092](#).

Summary: This gene is considered a member of a gene family predicted to encode transmembrane proteins. The specific function of this gene is unknown; however, expression in the inner ear suggests that it may be crucial for normal auditory function. Mutations in this gene may underlie hereditary disorders of balance and hearing.

FEATURES	Location/Qualifiers
source	1..3169 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="20" /map="20p13"
gene	1..3169 /gene="TMC2" /note="synonyms: C20orf145, dJ686C3.3" /db_xref="GeneID:117532" /db_xref="HGNC:16527" /db_xref="HPRD:09463" /db_xref="MIM:606707"
CDS	16..2736 /gene="TMC2" /go_component="integral to membrane; membrane" /note="transmembrane, cochlear expressed, 2" /codon_start=1 /product="transmembrane cochlear-expressed protein 2" /protein_id="NP_542789.2" /db_xref="GI:94536852" /db_xref="CCDS:CCDS13029.1" /db_xref="GeneID:117532" /db_xref="HGNC:16527" /db_xref="HPRD:09463" /db_xref="MIM:606707" /translation="MSHQVKGLKEEARGGVKGRVKS GSPHTGDRLGRRSSSKRALKAE GTPGRRGAQRSQKERAGGSPSPGSPRRKQTGRRRHREELGEQERGEAERTCEGRRKR ERASFQERTAAPKREKEIPRREEKSKRQKKPRSSSLASSASGGESLSEELAQILEQV EEKKKLIATMRSKPWPMAKKLTELRQAQEFVEKEYEGALGKGKGKQLYAYKMLMAKKWV KFKRDFDNFKTQCI PWEMKIKDIESHFGSSVASYFIFLRWYGVNLVLFGLIFGLVII PEVLGMMPYGSIPRKTVPRAEEKAMDFSVLWDFEGYIKYSALFYGYNNQRTIGWLR YRLPMAYFMVGVSVFGYSLII VIRSMASNTQGSGEGESDNFTFSFKMFTSWDYLIGN SETADNKYASITTSFKESIVDEQESNKEENIHLTRFLRVLANFLII CCLCGSGYLIYF VVKRSQQFSKMQNVSWYERNEVEIVMSLLGMFCPLFETIAALENYHPRTGLKWQLGR IFALFLGNLYTFLALMDDVHLKLANEETIKNITHWTLFNYYNSSGWNESVPRPPLHP ADVPRGSCWETAVGIEFMRLTVSDMLVTYITILLGDFLRACFVRFMNYCWCWDLEAGF PSYAEFDISGNVLGLIFNQGMIMWGSFYAPGLVGINVLRLLTSMYFQCWAVMSSNVPH ERVFKASRSNNFYMGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFSGKNRMYDVLQETI ENDFPTFLGKIFAFLANPGLIIPAILLMFLAIYYLNSVSKSLSRANAQLRKKIQVLR VEKSHKSVKGKATARDS EDTPKSSSKNATQLQLTKEETTPPSASQSQAMDKKAQGP GT SNSASRTTLPASGHLPI SRPPGIGPDSGHAPSQTHPWSASGKSAQRPPH"

ORIGIN

```

1 gcagtgcctgc tgacccatgag ccaccaggta aagggcctga aagagggaagc acgaggcgga
61 gtgaaagggc ggggtgaagag cggctctcca cacacagggtg acaggctggg aaggagatcc
121 tcaagcaagc gggctctcaa agccgagggg accccaggca ggcgcgagc tcagcgaagc
181 cagaaggagc gcgccggggg cagcccaagc ccgggggtctc cccggaggaa gcaaacaggg
241 cgcaggagac acagagaaga gctgggggag caggagcggg gcgaggcaga gaggacctgc
301 gagggcagga gaaagcgcg aagaggggccc tccttcagg agcggacagc agcccccagg
361 agggaaaagg agattccgag gagggaggag aagtcgaagc ggcagaaga acccagggtca
421 tcctccttgg cctccagtgc ctctgggtgg gagtcctgt ccgaggagga actggcccag
481 atcctggagc aggtggaaga aaaaaagaag ctcatgcca ccatgcggag caagccctgg
541 cccatggcga agaagctgac agagctcagg gagggccagg aatttgatga gaagatatga
601 ggtgccttgg gaaaggggaa aggcaagcaa ctatatgcct acaagatgct gatggccaag
661 aaatgggtca aatttaagag agactttgat aatttcaaga ctcaatgat cccctgggaa
721 atgaagatca aggacattga aagtcacttt ggttcttcag tggcatcgta tttcatcttt
781 ctccgatgga tgtatggagt taacctgtgc ctttttggt taatatttgg tctagtcata
841 atcccagagg tactgatggg catgccctat gggagtatcc ccagaaagac agtgcctcgg

```

```

901 gctgaggaag aaaaggccat ggatttttct gtcctttggg attttgaggg ctatatcaag
961 tactctgcac tcttctatgg ctactacaac aaccagagga ccacgggtg gctgaggtac
1021 cggctgccta tggcttactt tatggtgggg gtcagcgtgt tcggctacag cctgattatt
1081 gtcattcgat cgatggccag caatacccaa ggaagcacag gcgaagggga gagtgacaac
1141 ttcacattca gcttcaagat gttcaccagc tgggactacc tgatcgggaa ttcagagaca
1201 gctgataaca aatatgcatc catcaccacc agcttcaagg aatcaatagt ggatgaacaa
1261 gagagtaaca aagaagaaaa tatccatctg acaagatttc ttcgtgtcct ggccaacttt
1321 ctcatcatct gctgtttgtg tggaaagtggg tacctcattt actttgtggg taagcgatct
1381 cagcaattct ccaaaatgca gaatgtcagc tggatgaaa ggaatgaggt agagatcgtg
1441 atgtccctgc ttggaatgtt ttgtccccc ctgtttgaaa ccacgctgc cctggagaat
1501 taccacccac gcactggact gaagtggcag ctgggacgca tctttgact cttcctgggg
1561 aacctctaca catttctctt ggccctgatg gatgacgtcc acctcaagct tgctaataaa
1621 gagacaataa agaacatcac tcaactggact ctgtttaact attacaactc ttcctggttg
1681 aacgagagtg tcccccgacc accctgcac cctgcagatg tgccccgggg ttcctgtctg
1741 gagacagctg tgggcattga attcatgagg ctgacggtgt ctgacatgct ggtaacgtac
1801 atcaccatcc tgctggggga cttcctacgg gcttgttttg tgcggttcat gaactactgc
1861 tgggtgctggg acttgagggc tggatttcct tcatatgctg agtttgatat tagtggaat
1921 gtgctgggtt tgatcttcaa ccaaggaatg atctggatgg gctccttcta tgctccaggc
1981 ctgggtgggca ttaatgtgct gcgcctgctg acctccatgt acttccagtg ctgggagggtg
2041 atgagcagca acgtacccca tgaacgcgtg ttcaaagcct cccgatccaa caacttctac
2101 atgggcctcc tgctgctggt gctcttctc agcctcctgc cgggtggccta caccatcatg
2161 tccctccac cctcctttga ctgcgggccg ttcagtggga aaaacagaat gtacgatgtc
2221 ctccaagaga ccattgaaaa cgatttccca accttctgg gcaagatctt tgccttctc
2281 gccaatccag gctgatcat cccagccatc ctgctgatgt tcttggccat ttactacctg
2341 aactcagttt ccaaaagcct ttcccagct aatgcccagc tgaggaagaa aatccaagt
2401 ctccgtgaag ttgagaagag tcacaaatct gtaaaaggca aagccacagc cagagattca
2461 gaggacacac ctaaaagcag ctccaaaaat gccaccagc tccaactcac caaggaagag
2521 accactcctc cctctgccag ccaaagccag gccatggaca agaaggcgca gggccctggg
2581 acctccaatt ctgccagcag gaccacactg cctgcctctg gacacctcc tatatctcgg
2641 cccctggaa tcggaccaga ttctggccac gcccctctc agactcatcc gtggaggtca
2701 gcctctggaa agagtgtca gagacctccc cactgatggc taggactcca gggagcctcg
2761 accctagggc tgatctcaa gtacccagc ttcacacata ccaaaccaag gttctctccc
2821 ctctttctc tcacatacat gctctgtctc ctctcttgg atgcatgaac tttgattcct
2881 tcaggccctt gtcagctacc gaaggaggaa gacagtggc tcacctgtcc tttagggaag
2941 ctggagccat ctctgacta actgccctcc caaatatctt gggtcagaca gctctgaacc
3001 ccacgctcac agtggtcgac cttgcctccc gattttcgga gttggggaag ggccatgacc
3061 acctcgtag actttttcca tgggatacag tttaggacac gggtttctgc cagcttccct
3121 aaccaggagg gggatggaga agggcctaca tttctcaatc cagaggaag

```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Apr 11 2006 19:57:30

[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#)

Search for

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Display Show

Range: from to ☐ Reverse complemented strand Features:

☐ 1: [AF417580](#). Reports Homo sapiens tran...[gi:28642834]

[Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS AF417580 3169 bp mRNA linear PRI 05-MAR-2003
 DEFINITION Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds.
 ACCESSION AF417580
 VERSION AF417580.2 GI:28642834
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3169)
 AUTHORS Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S., Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N., Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Raizuddin,S., Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F., Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
 TITLE Dominant and recessive deafness caused by mutations of a novel gene, TMC1, required for cochlear hair-cell function
 JOURNAL Nat. Genet. 30 (3), 277-284 (2002)
 PUBMED [11850618](#)
 REFERENCE 2 (bases 1 to 3169)
 AUTHORS Kurima,K., Griffith,A.J. and Friedman,T.B.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02, Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 3169)
 AUTHORS Kurima,K., Griffith,A.J. and Friedman,T.B.
 TITLE Direct Submission
 JOURNAL Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02, Rockville, MD 20850, USA
 REMARK Sequence update by submitter
 COMMENT On Mar 3, 2003 this sequence version replaced gi:19223982.
 FEATURES
 source 1..3169
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="20"
 /map="20p13"
 /tissue_type="ear"
 gene 1..3169
 /gene="TMC2"
 CDS 16..2736
 /gene="TMC2"
 /codon_start=1
 /product="transmembrane channel-like protein 2"
 /protein_id="AAL86401.2"
 /db_xref="GI:28642835"
 /translation="MSHQVKGLKEEARGGVKGRVKSQSPHTGDRLGRRSSSKRALKAE"

GTPGRRGAQRSQKERAGGSPSPGSPRRKQTGRRRHREELGEQERGEAERTCEGRRKRDR
 ERASFQERTAAPKREKEIPRKEEKSQRQKKPRSSSLASSASGGESLSEELAQILEQV
 EEKKKLIATMRSKPWPMAKKLTELREAQEFVEKEYEGALGKGKGKQLYAYKMLMAKKWV
 KFKRDFDNFKTQCI PWEMKIKDIESHFGSSVASYFIFLRWYGVNLVLFGLIFGLVII
 PEVLGMMPYGSIPRKTVPRAEEKAMDFSVLWDFEGYIKYSALFYGYNNQRTIGWLR
 YRLPMAYFMVGVSVFGYSLIIVIRSMASNTQGSTGEGESDNFTFSFKMFTSWDYLIGN
 SETADNKYASITTSFKESIVDEQESNKEENIHLTRFLRVLANFLIICCLCGSGYLIYF
 VVKRSQQFSKMQNVSWYERNEVEIVMSLLGMFCPPLFETIAALENYHPRGTGLKWQLGR
 IFALFLGNLYTFLLALMDDVHLKLANEETIKNITHWTLFNYYNSSGWNESVPRPPLHP
 ADVPRGSCWETAVGIEFMRLTVSDMLVTYITILLGDFLRACFVRFMNYCWCWDLEAGF
 PSYAEFDISGNVLGLIFNQGMIMWGSFYAPGLVGINVLRLLTSMYFQCWAVMSSNVPH
 ERVFKASRSNNFYMGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFSGKNRMYDVLQETI
 ENDFPTFLGKIFAFLANPGLIIPAILLMFLAIYYLNSVSKSLSRANAQLRKKIQVLR
 VEKSHKSVKGKATARDS EDTPKSSSKNATQLQLTKEETPPSASQSQAMDKKAQGPPT
 SNSASRTTLPASGHLPISRPPGIGPDSGHAPSQTHPWSASGKSAQRPPH"

ORIGIN

1	gcagtgcctgc	tgaccatgag	ccaccagcta	aagggcctga	aagaggaagc	acgagggcga
61	gtgaaagggc	gggtgaagag	cggctctcca	cacacaggtg	acaggctggg	aaggagatcc
121	tcaagcaagc	gggctctcaa	agccgagggg	acccagaggc	ggcgcgagc	tcagcgaagc
181	cagaaggagc	gcgccggggg	cagcccaagc	ccgggggtctc	cccggaggaa	gcaaacaggg
241	cgcaggagac	acagagaaga	gctgggggag	caggagcggg	gcgaggcaga	gaggacctgc
301	gagggcagga	gaaagcgcg	cgagagggcc	tccttccagg	agcggacagc	agcccccagg
361	agggaaaagg	agattccgag	gaaggaggag	aagtcgaagc	ggcagaagaa	acccaggtca
421	tcctccttgg	cctccagtgc	ctctgggtggg	gagtcctctgt	ccgaggagga	actggcccag
481	atcctggagc	aggtggaaga	aaaaaagaag	ctcattgcca	ccatgcggag	caagccctgg
541	cccatggcga	agaagctgac	agagctcagg	gaggcccagg	aatttgtgga	gaagtatgaa
601	ggtgccttgg	gaaaggggaa	aggcaagcaa	ctatatgcct	acaagatgct	gatggccaag
661	aaatgggtca	aattttaagag	agactttgat	aatttcaaga	ctcaatgtat	cccctgggaa
721	atgaagatca	aggacattga	aagtcacttt	ggttcttcag	tggcatcgta	tttcatcttt
781	ctccgatgga	tgtatggagt	taaccttgct	ctttttggct	taatatattg	tctagtcata
841	atcccagagg	tactgatggg	catgccctat	gggagtattc	ccagaaagac	agtgcctcgg
901	gctgaggaag	aaaaggccat	ggatttttct	gtcctttggg	attttgaggg	ctatatcaag
961	tactctgcac	tcttctatgg	ctactacaac	aaccagagga	ccatcggttg	gctgaggtac
1021	cggctgccta	tggcttactt	tatggtgggg	gtcagcgtgt	tcggctacag	cctgattatt
1081	gtcattcgat	cgatggccag	caatacccaa	ggaagcacag	gcgaagggga	gagtgacaac
1141	ttcacattca	gcttcaagat	gttcaccagc	tgggactacc	tgatcgggaa	ttcagagaca
1201	gctgataaca	aatatgcac	catcaccacc	agcttcaagg	aatcaatagt	ggatgaacaa
1261	gagagtaaca	aagaagaaaa	tatccatctg	acaagatttc	ttcgtgtcct	ggccaacttt
1321	ctcatcatct	gctgtttgtg	tggaggtggg	tacctcattt	actttgtggt	taagcgatct
1381	cagcaattct	ccaaaatgca	gaatgtcagc	tggatgaaa	ggaatgaggt	agagatcgtg
1441	atgtccctgc	ttggaatgtt	ttgtccccct	ctgtttgaaa	ccatcgctgc	cctggagaat
1501	taccacccac	gcactggact	gaagtggcag	ctgggacgca	tctttgcact	cttctctggg
1561	aacctctaca	catttctctt	ggccctgatg	gatgacgtcc	acctcaagct	tgctaataaa
1621	gagacaataa	agaacatcac	tcactggact	ctgtttaact	attacaactc	ttctggttgg
1681	aacgagagtg	tcccccgacc	acccctgcac	cctgcagatg	tgccccgggg	ttctgtctgg
1741	gagacagctg	tgggcattga	attcatgagg	ctgacggtgt	ctgacatgct	ggtaacgtac
1801	atcacattcc	tgtctggggg	cttccctacg	gcttgttttg	tgcggttcat	gaactactgc
1861	tgggtgctgg	acttggaggc	tggatttcc	tcatatgctg	agtttgatat	tagtggaagt
1921	gtgctgggtt	tgatcttcaa	ccaaggaatg	atctggatgg	gctccttcta	tgctccaggc
1981	ctggtgggca	ttaatgtgct	gcgcctgctg	acctccatgt	acttccagtg	ctgggagggtg
2041	atgagcagca	acgtacccca	tgaacgcgtg	ttcaaagcct	cccgatccaa	caacttctac
2101	atgggcctcc	tgtctgtggt	gctcttcttc	agcctcctgc	cgggtggccta	caccatcatg
2161	tccctccac	cctcctttga	ctgcggggccg	ttcagtgagg	aaaacagaat	gtacgatgtc
2221	ctccaagaga	ccattgaaaa	cgatttccca	accttccctg	gcaagatctt	tgctttcctc
2281	gccaatccag	gcctgatcat	cccagccatc	ctgctgatgt	tcttggccat	ttactacctg
2341	aactcagttt	ccaaaagcct	ttcccagact	aatgcccagc	tgaggaagaa	aatccaagtg
2401	ctccgtgaag	ttgagaagag	tcacaaatct	gtaaaaggca	aagccacagc	cagagattca
2461	gaggacacac	ctaaaagcag	ctccaaaaat	gccacccagc	tccaactcac	caaggaagag
2521	accactcctc	cctctgccag	ccaaagccag	gccatggaca	agaaggcgca	gggcccctggg
2581	acctccaatt	ctgccagcag	gaccacactg	cctgcctctg	gacaccttcc	tatatctcgg
2641	ccccctggaa	tcggaccaga	ttctggccac	gccccatctc	agactcatcc	gtggaggctc
2701	gcctctggaa	agagtgtcca	gagacctccc	cactgacggc	taggactcca	gggagcctcg
2761	accctagggc	tgactctcaa	gtacccctag	ttcacacata	ccaaaccaag	gttctctccc
2821	ctctttcctc	tcacatacat	gctctgtctc	ctctcttggg	atgcatgaac	tttgattcct
2881	tcaggccctt	gtcagctacc	gaaggaggaa	gacagtggct	tcacctgtcc	tttaggggaag
2941	ctggagccat	ctctgcacta	actgcctccc	caaatatctt	ggttcagaca	gctctgaacc

3001 ccacgctcac agtgggtcgac cttgcctccc gattttcgga gttggggaag ggccatgacc
3061 accctcgtag actttttcca tgggatacag tttaggacac gggtttctgc cagcttcct
3121 aaccaggagg gggatggaga agggcctaca tttctcaatc cagaggaag

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Apr 11 2006 19:57:30

AF417580
LOCUS AF417580 3169 bp mRNA linear PRI 05-MAR-2003
DEFINITION Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds.
ACCESSION AF417580
VERSION AF417580.2 GI:28642834
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3169)
AUTHORS Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S., Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N., Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Raizuddin,S., Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F., Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
TITLE Dominant and recessive deafness caused by mutations of a novel gene, TMC1, required for cochlear hair-cell function
JOURNAL Nat. Genet. 30 (3), 277-284 (2002)
PUBMED 11850618
REFERENCE 2 (bases 1 to 3169)
AUTHORS Kurima,K., Griffith,A.J. and Friedman,T.B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02, Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 3169)
AUTHORS Kurima,K., Griffith,A.J. and Friedman,T.B.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02, Rockville, MD 20850, USA
REMARK Sequence update by submitter
COMMENT On Mar 3, 2003 this sequence version replaced gi:19223982.
FEATURES
source 1. .3169
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
/map="20p13"
/tissue_type="ear"
gene 1. .3169
/gene="TMC2"
CDS 16. .2736
/gene="TMC2"
/codon_start=1
/product="transmembrane channel-like protein 2"
/protein_id="AAL86401.2"
/db_xref="GI:28642835"
/translation="MSHQVKGLKEEARGGVKGRVKS GSPHTGDR LGRRSSSKRALKAE
GTPGRRGAQRSQKERAGGSPSPGSPRRKQTGRRRHREELGEQERGEAERTCEGRRKRD
ERASFQERTAAPKREKEIPRKEEKS KRQKKPRSSSLASSAGGESLSEEELAQILEQV
EEKKKLIATMRSKPWPMAKKLTLEAQEFVEKYEGALGKGKGLYAYKMLMAKKWV
KFKRDFDNFKTQCI PWEMKIKDIESHFGSSVASYFIFLRWYGVNLVLFGLIFGLVII
PEVLMGMPYGSIPRKTVPRAEEEKAMDFSVLWDFEGYIKYSALFYGYNNQRTIGWLR
YRLPMAYFMVGVSVFGYSLIIVIRSMASNTQGSGEGESDNFTFSFKMFTSWDYLGIN

SETADNKYASITTSFKESIVDEQESNKEENIHLTRFLRVLANFLIICCLCGSGYLIYF
VVKRSQQFSKMQNVSWYERNEVEIVMSLLGMFCPPLFETIAALENYHPRTGLKWQLGR
IFALFLGNLYTFLLALMDDVHLKLANEETIKNITHWTLFNYYNSSGWNESVPRPPLHP
ADVPRGSCWETAVGIEFMRLTVSDMLVTYITILLGDFLRACFVRFMNYCWCWDLEAGF
PSYAEFDISGNVLGLIFNQGMIWMGSFYAPGLVGINVLRLLTSMYFQCWAVMSSNVPH
ERVFKASRSNNFYMGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFSGKNRMYDVLQETI
ENDFPTFLGKIFAFLANPGLIIPAILLMFLAIYYLNSVSKSLSRANAQLRKKIQVLRE
VEKSHKSVKGKATARDESDTPKSSSKNATQLQLTKEETTPPSASQSQAMDKKAQGPPT
SNSASRTTLPASGHLPISRPPGIGPDSGHAPSQTHPWSASGKSAQRPPH"

ORIGIN

Query Match 100.0%; Score 3169; DB 8; Length 3169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCAGTGCTGCTGACCATGAGCCACCAGGTAAAGGGCCTGAAAGAGGAAGCACGAGGCGGA	60
Db	1	GCAGTGCTGCTGACCATGAGCCACCAGGTAAAGGGCCTGAAAGAGGAAGCACGAGGCGGA	60
Qy	61	GTGAAAGGGCGGGTGAAGAGCGGCTCTCCACACACAGGTGACAGGCTGGGAAGGAGATCC	120
Db	61	GTGAAAGGGCGGGTGAAGAGCGGCTCTCCACACACAGGTGACAGGCTGGGAAGGAGATCC	120
Qy	121	TCAAGCAAGCGGGCTCTCAAAGCCGAGGGGACCCAGGCAGGCGCGGAGCTCAGCGAAGC	180
Db	121	TCAAGCAAGCGGGCTCTCAAAGCCGAGGGGACCCAGGCAGGCGCGGAGCTCAGCGAAGC	180
Qy	181	CAGAAGGAGCGCGCCGGGGGCAGCCCAAGCCCGGGGTCTCCCCGAGGAAGCAAACAGGG	240
Db	181	CAGAAGGAGCGCGCCGGGGGCAGCCCAAGCCCGGGGTCTCCCCGAGGAAGCAAACAGGG	240
Qy	241	CGCAGGAGACACAGAGAAGAGCTGGGGGAGCAGGAGCGGGGCGAGGCAGAGAGGACCTGC	300
Db	241	CGCAGGAGACACAGAGAAGAGCTGGGGGAGCAGGAGCGGGGCGAGGCAGAGAGGACCTGC	300
Qy	301	GAGGGCAGGAGAAAGCGCGACGAGAGGGCCTCCTTCCAGGAGCGGACAGCAGCCCCAAAG	360
Db	301	GAGGGCAGGAGAAAGCGCGACGAGAGGGCCTCCTTCCAGGAGCGGACAGCAGCCCCAAAG	360
Qy	361	AGGGAAAAGGAGATTCCGAGGAAGGAGGAGAAGTCGAAGCGGCAGAAGAAACCCAGGTCA	420
Db	361	AGGGAAAAGGAGATTCCGAGGAAGGAGGAGAAGTCGAAGCGGCAGAAGAAACCCAGGTCA	420
Qy	421	TCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGAGTCCCTGTCCGAGGAGGAAGTGGCCAG	480
Db	421	TCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGAGTCCCTGTCCGAGGAGGAAGTGGCCAG	480
Qy	481	ATCCTGGAGCAGGTGGAAGAAAAAAGAAGCTCATTGCCACCATGCGGAGCAAGCCCTGG	540
Db	481	ATCCTGGAGCAGGTGGAAGAAAAAAGAAGCTCATTGCCACCATGCGGAGCAAGCCCTGG	540
Qy	541	CCCATGGCGAAGAAGCTGACAGAGCTCAGGGAGGCCAGGAATTTGTGGAGAAGTATGAA	600
Db	541	CCCATGGCGAAGAAGCTGACAGAGCTCAGGGAGGCCAGGAATTTGTGGAGAAGTATGAA	600

Qy	601	GGTGCCTTGGGAAAGGGGAAAGGCAAGCAACTATATGCCTACAAGATGCTGATGGCCAAG	660
Db	601		
	601	GGTGCCTTGGGAAAGGGGAAAGGCAAGCAACTATATGCCTACAAGATGCTGATGGCCAAG	660
Qy	661	AAATGGGTCAAATTTAAGAGAGACTTTGATAATTTCAAGACTCAATGTATCCCCTGGGAA	720
Db	661		
	661	AAATGGGTCAAATTTAAGAGAGACTTTGATAATTTCAAGACTCAATGTATCCCCTGGGAA	720
Qy	721	ATGAAGATCAAGGACATTGAAAGTCACTTTGGTTCCTCAGTGGCATCGTATTTTCATCTTT	780
Db	721		
	721	ATGAAGATCAAGGACATTGAAAGTCACTTTGGTTCCTCAGTGGCATCGTATTTTCATCTTT	780
Qy	781	CTCCGATGGATGTATGGAGTTAACCTTGTCTTTTTGGCTTAATATTTGGTCTAGTCATA	840
Db	781		
	781	CTCCGATGGATGTATGGAGTTAACCTTGTCTTTTTGGCTTAATATTTGGTCTAGTCATA	840
Qy	841	ATCCCAGAGGTACTGATGGGCATGCCCTATGGGAGTATTCCCAGAAAGACAGTGCCTCGG	900
Db	841		
	841	ATCCCAGAGGTACTGATGGGCATGCCCTATGGGAGTATTCCCAGAAAGACAGTGCCTCGG	900
Qy	901	GCTGAGGAAGAAAAGGCCATGGATTTTTCTGTCTTTGGGATTTTGAGGGCTATATCAAG	960
Db	901		
	901	GCTGAGGAAGAAAAGGCCATGGATTTTTCTGTCTTTGGGATTTTGAGGGCTATATCAAG	960
Qy	961	TACTCTGCACTCTTCTATGGCTACTACAACAACCAGAGGACCATCGGGTGGCTGAGGTAC	1020
Db	961		
	961	TACTCTGCACTCTTCTATGGCTACTACAACAACCAGAGGACCATCGGGTGGCTGAGGTAC	1020
Qy	1021	CGGCTGCCTATGGCTTACTTTATGGTGGGGGTGAGCGTGTTCGGCTACAGCCTGATTATT	1080
Db	1021		
	1021	CGGCTGCCTATGGCTTACTTTATGGTGGGGGTGAGCGTGTTCGGCTACAGCCTGATTATT	1080
Qy	1081	GTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGGCGAAGGGGAGAGTGACAAC	1140
Db	1081		
	1081	GTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGGCGAAGGGGAGAGTGACAAC	1140
Qy	1141	TTACATTCAGCTTCAAGATGTTACACAGCTGGGACTACCTGATCGGGAATTCAGAGACA	1200
Db	1141		
	1141	TTACATTCAGCTTCAAGATGTTACACAGCTGGGACTACCTGATCGGGAATTCAGAGACA	1200
Qy	1201	GCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAA	1260
Db	1201		
	1201	GCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAA	1260
Qy	1261	GAGAGTAACAAAGAAGAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTT	1320
Db	1261		
	1261	GAGAGTAACAAAGAAGAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTT	1320
Qy	1321	CTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTCATTTACTTTGTGGTTAAGCGATCT	1380
Db	1321		
	1321	CTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTCATTTACTTTGTGGTTAAGCGATCT	1380
Qy	1381	CAGCAATTCTCCAAAATGCAGAATGTCAGCTGGTATGAAAGGAATGAGGTAGAGATCGTG	1440
Db	1381		
	1381	CAGCAATTCTCCAAAATGCAGAATGTCAGCTGGTATGAAAGGAATGAGGTAGAGATCGTG	1440

Qy	1441	ATGTCCCTGCTTGAATGTTTTGTCCCCCTCTGTTTGAAACCATCGCTGCCCTGGAGAAT	1500
Db	1441	ATGTCCCTGCTTGAATGTTTTGTCCCCCTCTGTTTGAAACCATCGCTGCCCTGGAGAAT	1500
Qy	1501	TACCACCCACGCACTGGACTGAAGTGGCAGCTGGGACGCATCTTTGCACTCTTCCTGGGG	1560
Db	1501	TACCACCCACGCACTGGACTGAAGTGGCAGCTGGGACGCATCTTTGCACTCTTCCTGGGG	1560
Qy	1561	AACCTCTACACATTTCTCTTGGCCCTGATGGATGACGTCCACCTCAAGCTTGCTAATGAA	1620
Db	1561	AACCTCTACACATTTCTCTTGGCCCTGATGGATGACGTCCACCTCAAGCTTGCTAATGAA	1620
Qy	1621	GAGACAATAAAGAACATCACTCACTGGACTCTGTTTAACTATTACAACCTCTTCTGGTTGG	1680
Db	1621	GAGACAATAAAGAACATCACTCACTGGACTCTGTTTAACTATTACAACCTCTTCTGGTTGG	1680
Qy	1681	AACGAGAGTGTCCCCCGACCACCCCTGCACCCTGCAGATGTGCCCCGGGGTTCTTGCTGG	1740
Db	1681	AACGAGAGTGTCCCCCGACCACCCCTGCACCCTGCAGATGTGCCCCGGGGTTCTTGCTGG	1740
Qy	1741	GAGACAGCTGTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAACGTAC	1800
Db	1741	GAGACAGCTGTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAACGTAC	1800
Qy	1801	ATCACCATCCTGCTGGGGGACTTCCTACGGGCTTGTTTTGTGCGGTTTCATGAACACTGC	1860
Db	1801	ATCACCATCCTGCTGGGGGACTTCCTACGGGCTTGTTTTGTGCGGTTTCATGAACACTGC	1860
Qy	1861	TGGTGCTGGGACTTGGAGGCTGGATTTCTTCATATGCTGAGTTTGATATTAGTGGAAT	1920
Db	1861	TGGTGCTGGGACTTGGAGGCTGGATTTCTTCATATGCTGAGTTTGATATTAGTGGAAT	1920
Qy	1921	GTGCTGGGTTTGATCTTCAACCAAGGAATGATCTGGATGGGCTCCTTCTATGCTCCAGGC	1980
Db	1921	GTGCTGGGTTTGATCTTCAACCAAGGAATGATCTGGATGGGCTCCTTCTATGCTCCAGGC	1980
Qy	1981	CTGGTGGGCATTAATGTGCTGCGCCTGCTGACCTCCATGTACTTCCAGTGCTGGGCGGTG	2040
Db	1981	CTGGTGGGCATTAATGTGCTGCGCCTGCTGACCTCCATGTACTTCCAGTGCTGGGCGGTG	2040
Qy	2041	ATGAGCAGCAACGTACCCCATGAACGCGTGTTCAAAGCCTCCCGATCCAACAACCTTCTAC	2100
Db	2041	ATGAGCAGCAACGTACCCCATGAACGCGTGTTCAAAGCCTCCCGATCCAACAACCTTCTAC	2100
Qy	2101	ATGGGCCTCCTGCTGCTGGTGCTCTTCTCAGCCTCCTGCCGGTGGCCTACACCATCATG	2160
Db	2101	ATGGGCCTCCTGCTGCTGGTGCTCTTCTCAGCCTCCTGCCGGTGGCCTACACCATCATG	2160
Qy	2161	TCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGGGAAAAACAGAATGTACGATGTC	2220
Db	2161	TCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGGGAAAAACAGAATGTACGATGTC	2220
Qy	2221	CTCCAAGAGACCATTGAAAACGATTTCCCAACCTTCCTGGGCAAGATCTTTGCTTTCTC	2280
Db	2221	CTCCAAGAGACCATTGAAAACGATTTCCCAACCTTCCTGGGCAAGATCTTTGCTTTCTC	2280

Qy	2281	GCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTGATGTTCTTGGCCATTTACTACCTG	2340
Db	2281	GCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTGATGTTCTTGGCCATTTACTACCTG	2340
Qy	2341	AACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGAAGAAAATCCAAGTG	2400
Db	2341	AACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGAAGAAAATCCAAGTG	2400
Qy	2401	CTCCGTGAAGTTGAGAAGAGTCACAAATCTGTAAAAGGCAAAGCCACAGCCAGAGATTCA	2460
Db	2401	CTCCGTGAAGTTGAGAAGAGTCACAAATCTGTAAAAGGCAAAGCCACAGCCAGAGATTCA	2460
Qy	2461	GAGGACACACCTAAAAGCAGCTCCAAAAATGCCACCCAGCTCCAACCTACCAAGGAAGAG	2520
Db	2461	GAGGACACACCTAAAAGCAGCTCCAAAAATGCCACCCAGCTCCAACCTACCAAGGAAGAG	2520
Qy	2521	ACCACTCCTCCCTCTGCCAGCCAAAGCCAGGCCATGGACAAGAAGGCGCAGGGCCCTGGG	2580
Db	2521	ACCACTCCTCCCTCTGCCAGCCAAAGCCAGGCCATGGACAAGAAGGCGCAGGGCCCTGGG	2580
Qy	2581	ACCTCCAATTCTGCCAGCAGGACCACACTGCCTGCCTCTGGACACCTTCCTATATCTCGG	2640
Db	2581	ACCTCCAATTCTGCCAGCAGGACCACACTGCCTGCCTCTGGACACCTTCCTATATCTCGG	2640
Qy	2641	CCCCCTGGAATCGGACCAGATTCTGGCCACGCCCCATCTCAGACTCATCCGTGGAGGTCA	2700
Db	2641	CCCCCTGGAATCGGACCAGATTCTGGCCACGCCCCATCTCAGACTCATCCGTGGAGGTCA	2700
Qy	2701	GCCTCTGGAAGAGTGCTCAGAGACCTCCCCACTGACGGCTAGGACTCCAGGGAGCCTCG	2760
Db	2701	GCCTCTGGAAGAGTGCTCAGAGACCTCCCCACTGACGGCTAGGACTCCAGGGAGCCTCG	2760
Qy	2761	ACCCTAGGGCTGATCCTCAAGTACCCAGTTTCACACATACCAAACCAAGGTTCTCTCCC	2820
Db	2761	ACCCTAGGGCTGATCCTCAAGTACCCAGTTTCACACATACCAAACCAAGGTTCTCTCCC	2820
Qy	2821	CTCTTTCTCTCACATACATGCTCTGTCTCCTCTCTTGGGAATGCATGAACCTTTGATTCT	2880
Db	2821	CTCTTTCTCTCACATACATGCTCTGTCTCCTCTCTTGGGAATGCATGAACCTTTGATTCT	2880
Qy	2881	TCAGGCCCTTGTCAGCTACCGAAGGAGGAAGACAGTGGCTTCACCTGTCTTTAGGGAAG	2940
Db	2881	TCAGGCCCTTGTCAGCTACCGAAGGAGGAAGACAGTGGCTTCACCTGTCTTTAGGGAAG	2940
Qy	2941	CTGGAGCCATCTCTGCACTAACTGCCCTCCCAAATATCTTGGTTCAGACAGCTCTGAACC	3000
Db	2941	CTGGAGCCATCTCTGCACTAACTGCCCTCCCAAATATCTTGGTTCAGACAGCTCTGAACC	3000
Qy	3001	CCACGCTCACAGTGGTCGACCTTGCTCCCGATTTTCGGAGTTGGGGAAGGGCCATGACC	3060
Db	3001	CCACGCTCACAGTGGTCGACCTTGCTCCCGATTTTCGGAGTTGGGGAAGGGCCATGACC	3060
Qy	3061	ACCCTCGTAGACTTTTTCCATGGGATACAGTTTAGGACACGGGTTTCTGCCAGCTTCCCT	3120
Db	3061	ACCCTCGTAGACTTTTTCCATGGGATACAGTTTAGGACACGGGTTTCTGCCAGCTTCCCT	3120

Qy	3121	AACCAGGAGGGGGATGGAGAAGGGCCTACATTTCTCAATCCAGAGGAAG	3169
Db	3121	AACCAGGAGGGGGATGGAGAAGGGCCTACATTTCTCAATCCAGAGGAAG	3169



All Databases

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

My NCBI

[\[Sign In\]](#) [\[Register\]](#)

Search for [Save Search](#)

Limits

Preview/Index

History

Clipboard

Details

Display

Show

[About Entrez](#)

[Entrez Nucleotide](#)
[Help](#) | [FAQ](#)

[Entrez Tools](#)

[Check sequence](#)
[revision history](#)

[LinkOut](#)

[My NCBI \(Cubby\)](#)

[Related resources](#)
[BLAST](#)

[Reference sequence](#)
[project](#)

[Search for Genes](#)

[Submit to GenBank](#)

[Search for full length](#)
[cDNAs](#)

All: 1

bacteria: 0

mRNA: 0

RefSeq: 0



Show only records from: [CoreNucleotide](#) (1), [EST](#) (0), [GSS](#) (0). [\[What's this?\]](#)

☐ 1:

[NM_080751](#)

Reports

gi|20304092|ref|NM_080751.1|[20304092]

The record has been replaced by [NM_080751.2](#)

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 22 2006 06:31:57